

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING A NOVEL HUMAN PHOSPHATASE, BMY_HPP13

<130> D0149 NP

<160> 40

<170> PatentIn version 3.2

<210> 1

<211> 989

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(763)

<400> 1

ctctctcagc ttcagagggaa aaaaa atg gtt gta gat ttc tgg act tgg gag
Met Val Val Asp Phe Trp Thr Trp Glu
1 5

cag aca ttt caa gaa cta atc caa gag gca aaa ccc cgg gcc aca tgg
Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala Lys Pro Arg Ala Thr Trp
10 15 20 25

acg ctg aag ttg gat ggc aac ctt cag cta gac tgc ctg gct caa ggg
Thr Leu Lys Leu Asp Gly Asn Leu Gln Leu Asp Cys Leu Ala Gln Gly
30 35 40

tgg aag caa tac caa cag aga gca ttt ggc tgg ttc cgg tgg tcc tcc
Trp Lys Gln Tyr Gln Gln Arg Ala Phe Gly Trp Phe Arg Cys Ser Ser
45 50 55

tgc cag cga agt tgg gct tcc gcc caa gtg cag att ctg tgc cac acg
Cys Gln Arg Ser Trp Ala Ser Ala Gln Val Gln Ile Leu Cys His Thr
60 65 70

tac tgg gag cac tgg aca tcc cag ggt cag gtg cgt atg agg ctc ttt
Tyr Trp Glu His Trp Thr Ser Gln Gly Gln Val Arg Met Arg Leu Phe
75 80 85

ggc caa agg tgc cag aag tgc tcc tgg tcc caa tat gag atg cct gag
Gly Gln Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu
90 95 100 105

ttc tcc tgc gat agc acc atg agg att ctg agc aac ctg gtg cag cat
Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu Val Gln His
110 115 120

ata ctg aag aaa tac tat gga aat ggc acg agg aag tct cca gaa atg
Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met

52

100

148

196

244

292

340

388

436

125	130	135	
cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac aca gcc aat Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp Thr Ala Asn 140	145	150	484
tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta aaa agc tgc Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu Lys Ser Cys 155	160	165	532
atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag act ggg aat Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys Thr Gly Asn 170	175	180	580
tcc tca cct gga att ggt gct gtg tac ctc gca aac caa gcc aag aac Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln Ala Lys Asn 190	195	200	628
cag tca gct gag gca aaa gag gct aag ggg agt ggg tat gag aaa tta Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu 205	210	215	676
ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc ttt att ttg Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val Phe Ile Leu 220	225	230	724
ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa tgatgaaaaat Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu 235	240	245	773
aggcttgcctt ctttctctta ttttaattcc atggtagtca atgaactggc tgccacttta atataactga aaattcattt tgagaccaag caggatcaag tttgtagaat aaacactggt ttccttagccatccatctgaaa acagttatgaa acatgaccaa gtacataatg gattttagaa taaatattgt cgaatttgcta aaaaaaaaaa aaaaag			833 893 953 989
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Met Val Val Asp Phe Trp Thr Trp Glu Gln Thr Phe Gln Glu Leu Ile 1	5	10	15
Gln Glu Ala Lys Pro Arg Ala Thr Trp Thr Leu Lys Leu Asp Gly Asn 20	25	30	
Leu Gln Leu Asp Cys Leu Ala Gln Gly Trp Lys Gln Tyr Gln Gln Arg 35	40	45	

Ala Phe Gly Trp Phe Arg Cys Ser Ser Cys Gln Arg Ser Trp Ala Ser
50 55 60

Ala Gln Val Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser
65 70 75 80

Gln Gly Gln Val Arg Met Arg Leu Phe Gly Gln Arg Cys Gln Lys Cys
85 90 95

Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser Ser Asp Ser Thr Met
100 105 110

Arg Ile Leu Ser Asn Leu Val Gln His Ile Leu Lys Lys Tyr Tyr Gly
115 120 125

Asn Gly Thr Arg Lys Ser Pro Glu Met Pro Val Ile Leu Glu Val Ser
130 135 140

Leu Glu Gly Ser His Asp Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly
145 150 155 160

Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys Ser
165 170 175

Leu Leu Pro His Leu Lys Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala
180 185 190

Val Tyr Leu Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu
195 200 205

Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp
210 215 220

Pro Leu Asn Ile Cys Val Phe Ile Leu Leu Leu Val Phe Ile Val Val
225 230 235 240

Lys Cys Phe Thr Ser Glu
245

<210> 3
<211> 624
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
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Met	Arg	Val	Ile	Glu	Gly	Lys	Gly	Phe	Ala	Gln	Gly	Leu	Pro	Asp	Val	
1			5						10				15			

aac tgg atc ttc aac cca ggt tcc ggt gtt cct cct gcc agc gaa gtt

Asn	Trp	Ile	Phe	Asn	Pro	Gly	Ser	Gly	Val	Pro	Pro	Ala	Ser	Glu	Val	96
									25				30			
20																

ggg ctt ccg ccc aag tgc aga ttc tgt gcc aca cgt act ggg agc act

Gly	Leu	Pro	Pro	Lys	Cys	Arg	Phe	Cys	Ala	Thr	Arg	Thr	Gly	Ser	Thr	144
35							40			45						

gga cat ccc agg gtc agg tgc cag aag tgc tcc tgg tcc caa tat gag

Gly	His	Pro	Arg	Val	Arg	Cys	Gln	Lys	Cys	Ser	Trp	Ser	Gln	Tyr	Glu	192
50						55				60						

atg cct gag ttc tcc tcg gat agc acc atg agg att ctg agc aac ctg

Met	Pro	Glu	Phe	Ser	Ser	Asp	Ser	Thr	Met	Arg	Ile	Leu	Ser	Asn	Leu	240
									65		75		80			
						70										

gtg cag cat ata ctg aag aaa tac tat gga aat ggc acg agg aag tct

Val	Gln	His	Ile	Leu	Lys	Tyr	Tyr	Gly	Asn	Gly	Thr	Arg	Lys	Ser	288
									85		90		95		

cca gaa atg cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac

Pro	Glu	Met	Pro	Val	Ile	Leu	Glu	Val	Ser	Leu	Glu	Gly	Ser	His	Asp	336
									100		105		110			

aca gcc aat tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta

Thr	Ala	Asn	Cys	Glu	Ala	Cys	Thr	Leu	Gly	Ile	Cys	Gly	Gln	Gly	Leu	384
									115		120		125			

aaa agc tgc atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag

Lys	Ser	Cys	Met	Thr	Lys	Pro	Ser	Lys	Ser	Leu	Leu	Pro	His	Leu	Lys	432
									130		135		140			

act ggg aat tcc tca cct gga att ggt gct gtg tac ctc gca aac caa

Thr	Gly	Asn	Ser	Ser	Pro	Gly	Ile	Gly	Ala	Val	Tyr	Leu	Ala	Asn	Gln	480
									145		150		155		160	

gcc aag aac cag tca gct gag gca aaa gag gct aag ggg agt ggg tat

Ala	Lys	Asn	Gln	Ser	Ala	Glu	Ala	Lys	Glu	Ala	Lys	Gly	Ser	Gly	Tyr	528
									165		170		175			

gag aaa tta ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc

Glu	Lys	Leu	Gly	Pro	Ser	Arg	Asp	Pro	Asp	Pro	Leu	Asn	Ile	Cys	Val	576
									180		185		190			

ttt att ttg ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa

Phe	Ile	Leu	Leu	Val	Phe	Ile	Val	Val	Lys	Cys	Phe	Thr	Ser	Glu	624

195

200

205

<210> 4
<211> 208
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<213> Homo sapiens

<400> 4

Met Arg Val Ile Glu Gly Lys Gly Phe Ala Gln Gly Leu Pro Asp Val
1 5 10 15

Asn Trp Ile Phe Asn Pro Gly Ser Gly Val Pro Pro Ala Ser Glu Val
20 25 30

Gly Leu Pro Pro Lys Cys Arg Phe Cys Ala Thr Arg Thr Gly Ser Thr
35 40 45

Gly His Pro Arg Val Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu
50 55 60

Met Pro Glu Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu
65 70 75 80

Val Gln His Ile Leu Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser
85 90 95

Pro Glu Met Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp
100 105 110

Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu
115 120 125

Lys Ser Cys Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys
130 135 140

Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln
145 150 155 160

Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr
165 170 175

Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val
180 185 190

Phe Ile Leu Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu
195 200 205

<210> 5
<211> 7
<212> PRT
<213> HOMO SAPIENS

<400> 5

Asp Tyr Ile Asn Ala Ser Asn
1 5

<210> 6
<211> 6
<212> PRT
<213> HOMO SAPIENS

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> wherein "X" equals any naturally occurring amino acid.

<400> 6

Cys Xaa Xaa Tyr Trp Pro
1 5

<210> 7
<211> 9
<212> PRT
<213> HOMO SAPIENS

<220>
<221> MISC_FEATURE
<222> (5)..(8)
<223> wherein "X" equals any naturally occurring amino acid.

<400> 7

Ile Val Val Met Xaa Xaa Xaa Xaa Glu
1 5

<210> 8
<211> 8
<212> PRT
<213> HOMO SAPIENS

<400> 8

Asp Asn Tyr Ile Asn Ala Ser Asn
1 5

<210> 9
<211> 6
<212> PRT
<213> HOMO SAPIENS

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> wherein "X" equals any naturally occurring amino acid.

<400> 9

Cys Xaa Xaa Tyr Trp Pro
1 5

<210> 10
<211> 9
<212> PRT
<213> HOMO SAPIENS

<220>
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<223> wherein "X" equals any naturally occurring amino acid.

<400> 10

Ile Val Val Met Xaa Xaa Xaa Xaa Glu
1 5

<210> 11
<211> 566
<212> PRT
<213> HOMO SAPIENS

<400> 11

Met Glu Val Pro Gln Pro Glu Pro Ala Pro Gly Ser Ala Leu Ser Pro
1 5 10 15

Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
20 25 30

Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
35 40 45

Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
50 55 60

Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala
65 70 75 80

Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly
85 90 95

Leu Cys Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln
100 105 110

Thr Phe Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu
115 120 125

Gln Phe Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly
130 135 140

His Ser Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly
145 150 155 160

Arg Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu
165 170 175

Asp Lys Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr
180 185 190

His Pro Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu
195 200 205

Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser
210 215 220

Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly
225 230 235 240

Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly
245 250 255

Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp Asp Asp Ala Val Pro
260 265 270

Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu Val Lys Thr Leu Glu

275

280

285

Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser Lys Cys Gln Arg Leu
290 295 300

Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile Arg Pro Ile Leu Lys
305 310 315 320

Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg
325 330 335

Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln Glu Ala Glu Glu Pro
340 345 350

Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys His Asp Glu Ile Glu
355 360 365

Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile Gly Asp Tyr Ser Lys
370 375 380

Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp Leu Lys Tyr
385 390 395 400

Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys Phe Ser Asn
405 410 415

Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro Tyr Glu Tyr
420 425 430

Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu Glu Arg Asp
435 440 445

Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys Ser Leu Asp
450 455 460

Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser Glu Arg Gly
465 470 475 480

Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala Val Asn Asp
485 490 495

Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys Gly Gly Tyr
500 505 510

Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro Gln Asp Tyr
515 520 525

Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys Thr Phe Arg
530 535 540

Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg Glu Leu Cys
545 550 555 560

Ser Arg Leu Gln Asp Gln
565

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<213> Homo sapiens

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gccagaggcgtcgtaaaggc attttctgac gtttgaaaaa caacgccaca attgagaaat 120
cgacgacggt cggtcgagat ggtatgatgc gtaataaact atcccccaag attcgagggt 180
cgacgaactgggagagt gatgcacgcgc ccaatgtatc cgtaggatta tg 232

<210> 13
<211> 21
<212> DNA
<213> Homo sapiens

<400> 13
tcaagggtgg aagcaatacc a 21

<210> 14
<211> 18
<212> DNA
<213> Homo sapiens

<400> 14
cttcgctggc aggaggaa 18

<210> 15
<211> 24
<212> DNA
<213> Homo sapiens

<400> 15

ccggaaccag ccaaatgctc tctg

24

<210> 16
<211> 525
<212> PRT
<213> HOMO SAPIENS

<400> 16

Met Lys Ser Arg Arg Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala
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Glu Asn Leu Leu Leu Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg
20 25 30

Pro Ser Lys Ser Asn Pro Gly Asp Leu Thr Leu Ser Val Arg Arg Asn
35 40 45

Gly Ala Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp
50 55 60

Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr
65 70 75 80

Tyr Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile
85 90 95

Glu Leu Lys Tyr Pro Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp
100 105 110

Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu
115 120 125

Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro
130 135 140

Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser
145 150 155 160

Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln Glu
165 170 175

Leu Lys Tyr Asp Val Gly Gly Glu Arg Phe Asp Ser Leu Thr Asp
180 185 190

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
195 200 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
210 215 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
225 230 235 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
245 250 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
275 280 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr
290 295 300 320

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
370 375 380 400

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Gly Asn Thr Glu Arg Thr Val Trp
405 410 415

Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro
420 425 430

Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser
435 440 445

Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly
450 455 460

Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg
465 470 475 480

Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr Ile Gln Met
485 490 495

Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg
500 505 510

Ser Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr Leu
515 520 525

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<212> PRT

<213> Homo sapiens

<400> 17

Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met
1 5 10

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<400> 18

Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala
1 5 10

<210> 19

<211> 13

<212> PRT

<213> Homo sapiens

<400> 19

Pro Arg Ala Thr Trp Thr Leu Lys Leu Asp Gly Asn Leu
1 5 10

<210> 20
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<212> PRT
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<400> 20

Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu
1 5 10

<210> 21
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<213> Homo sapiens

<400> 21

Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met Pro
1 5 10

<210> 22
<211> 14
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<400> 22

Trp Thr Trp Glu Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala
1 5 10

<210> 23
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<212> PRT
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<400> 23

Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser Gln
1 5 10

<210> 24
<211> 14
<212> PRT
<213> Homo sapiens

<400> 24

Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser
1 5 10

<210> 25
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<212> PRT
<213> Homo sapiens

<400> 25

Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser
1 5 10

<210> 26
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<213> Homo sapiens

<400> 26

Glu Val Ser Leu Glu Gly Ser His Asp Thr Ala Asn Cys Glu Ala Cys
1 5 10 15

<210> 27
<211> 16
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<400> 27

Gly Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys
1 5 10 15

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<211> 80
<212> DNA
<213> Homo sapiens

<400> 28
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tcccccttagc ctctttgcc

60

80

<210> 29
<211> 20
<212> DNA
<213> Bacteriophage T7

<400> 29
taatacgact cactataggg

20

<210> 30
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<212> DNA
<213> Bacteriophage SP6

<400> 30
atttaggtga cactatag

18

<210> 31
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<213> Homo sapiens

<400> 31
tcccaatatg agatgcctga

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<210> 32
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<400> 32
agctgactgg ttcttggctt

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<213> bacteriophage T7

<400> 33

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 34
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tctcccgac tcctgaggac acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa tgccaaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtagc aagtgcagg tctccaacaa agccctccca acccccacatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catgccgtg gagtggaga gcaatggca gccggagaac aactacaaga	540		
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg	600		
acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtgatgcat gaggctctgc	660		
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc	720		
gactctagag gat	733		
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gcagcagcgg ccgcgaggca aaaccccgaaa ccacatgg	38		
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Pro Leu Asn Ile Cys Val Phe Ile Leu Leu Leu Val Phe Ile Val Val			
1	5	10	15

Lys Cys Phe

<210> 40

<211> 297

<212> PRT

<213> Homo sapiens

<400> 40

Glu Met Glu Lys Glu Phe Glu Gln Ile Asp Lys Ser Gly Ser Trp Ala
1 5 10 15

Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys Arg
20 25 30

Val Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp Val
35 40 45

Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn Asp
50 55 60

Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser Tyr
65 70 75 80

Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp Glu
85 90 95

Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg Val
100 105 110

Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys Glu
115 120 125

Glu Lys Glu Met Ile Phe Glu Asp Thr Asn Leu Lys Leu Thr Leu Ile
130 135 140

Ser Glu Asp Ile Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu Glu
145 150 155 160

Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr Thr
165 170 175

Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu Asn
180 185 190

Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His Gly
195 200 205

Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr Phe
210 215 220

Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp Pro
225 230 235 240

Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe Arg
245 250 255

Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu Ala
260 265 270

Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln Asp
275 280 285

Gln Trp Lys Glu Leu Ser His Glu Asp
290 295